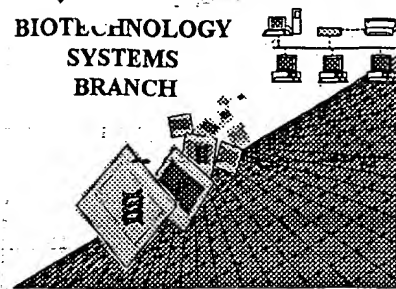


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/716,964

Source: OIPK

Date Processed by STIC: 12/7/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/7/96 964

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213> Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220> Feature (NEW RULES) Sequence(s) ____ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000
 TIME: 07:50:03

Input Set : A:\R10301.app
 Output Set: N:\CRF3\12072000\I716964.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: O'Donnell, Michael E.
 4 Yushakov, Alexander
 5 Yacheva, Olga
 6 Jermolami, David
 7 Bruck, Irina
 8 Karkhan, John
 10 <120> TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
 11 FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
 12 USE THEREOF
 14 <130> FILE REFERENCE: 22221/1030
 C--> 16 <140> CURRENT APPLICATION NUMBER: US/09/716,964
 C--> 17 <141> CURRENT FILING DATE: 2000-11-21
 19 <150> PRIOR APPLICATION NUMBER: 60/143,202
 20 <151> PRIOR FILING DATE: 1997-04-08
 22 <150> PRIOR APPLICATION NUMBER: 08/823,407
 23 <151> PRIOR FILING DATE: 1997-04-08
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 26 <151> PRIOR FILING DATE: 1998-04-08
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 33 <211> LENGTH: 2007
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 35 <213> ORGANISM: Thermus thermophilus
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PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

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62 ttggggtggg aggaaggtct cctcgtctcty gagggaqaaa aaaaaagcct gagcccaagg 1500
63 ccccccggg cccacctcc tgaagggccc gcaccccgag gccctcccgq ggaaggagta 1560
64 gttggggagg agcggcgga ggaaggcccg gaggagggct tgagaggggt ggttcgctc 1620
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66 cccctgagcc aagacagat aggggtact ggtatataat ggggcatga cccggaccac 1740
67 ccacctcgga caagagacc tggacaacat cctcaaggcc ctcccccga ttgaaggcca 1800
68 ggtgcggggg ctccagaaga tgggtggcga gggccggccc tgcgacgagg tctccacca 1860
69 gttgaccgcc accaagaagg ccattggagg gggggccccc ctgactctcc aagatttct 1920
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71 cggcaccatg ctgaagaact tcatcta 2007
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75 <211> LENGTH: 529
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77 <213> ORGANISM: Thermus thermophilus
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83 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
84 20 25 30
86 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
87 35 40 45
89 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
90 50 55 60
92 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
93 65 70 75 80
95 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
96 85 90 95
98 Val Glu Asp Val Arg Glu Leu Arg Glu Arg Ile His Leu Ala Pro Leu
99 100 105 110
101 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Glu Ala His Met Leu Ser
102 115 120 125
104 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Gln Pro Pro Pro
105 130 135 140
107 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Glu Arg Met Pro Pro
108 145 150 155 160
110 Thr Ile Leu Ser Arg Thr Glu His Phe Arg Phe Arg Arg Leu Thr Glu
111 165 170 175
113 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
114 180 185 190
116 Glu Ala Glu Glu Glu Ala Leu Leu Leu Leu Ala Arg Leu Ala Asp Gly
117 195 200 205
119 Ala Leu Arg Asp Ala Glu Ser Leu Leu Glu Arg Phe Leu Leu Leu Glu
120 210 215 220
122 Gly Pro Leu Thr Arg Lys Glu Val Glu Arg Ala Leu Gly Ser Pro Pro
123 225 230 235 240
125 Gly Thr Gly Val Ala Glu Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
126 245 250 255

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:03

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Output Set: N:\CRF3\12072000\I716964.raw

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132          275          280          285
134 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Glu
135          290          295          300
137 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
138 305          310          315          320
139 Ala Arg Arg Ser Asp Ala Leu Ser Leu Glu Val Ala Leu Leu Glu Ala
141          325          330          335
143 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Glu Pro Thr Gly Ala Pro
144          340          345          350
146 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
147          355          360          365
149 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
150          370          375          380
152 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
153 385          390          395          400
155 Pro Glu Val Arg Glu Gly Glu Leu Cys Leu Ala Phe Pro Glu Asp Lys
156          405          410          415
158 Ala Phe His Tyr Arg Lys Ala Ser Glu Glu Cys Val Arg Leu Leu Pro
159          420          425          430
161 Leu Ala Glu Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
162          435          440          445
164 Gly Glu Lys Lys Ser Leu Ser Pro Arg Pro Arg Pro Ala Pro Pro Pro
165          450          455          460
167 Glu Ala Pro Ala Pro Pro Gly Pro Pro Glu Glu Val Glu Ala Glu
168 465          470          475          480
170 Glu Ala Ala Glu Glu Ala Pro Glu Glu Ala Leu Arg Arg Val Val Arg
171          485          490          495
173 Leu Leu Gly Gly Arg Val Leu Trp Val Arg Arg Pro Arg Thr Arg Glu
174          500          505          510
176 Ala Pro Glu Glu Glu Pro Leu Ser Glu Asp Glu Ile Gly Gly Thr Gly
177          515          520          525
179 Ile
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185 <212> TYPE: DNA
186 <213> ORGANISM: Thermus thermophilus
188 <400> SEQUENCE: 3
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191 ttctccgccc ccaagggcgt ggcaagacc accacggcga gctctctccc catggcgtg 180
192 gggtagcagg ggaagacccc cccctgccc gttctgcccc actgcagagc ggtgcagagg 240
193 ggcgcccacc cggacgttgt ggacattgac gcgcgcagca acaactccgt ggaggacgtg 300
194 cgggagctga gggaaaggat ccacctcgcc cccctctctg ccccagga ggtcttcttc 360
195 ctggacgagg ccacatgct ctccaaaagc gcttccacg cctctctcaa gacctggag 420
196 gagccccccc cccagctct ctcgtcttc gccacaccc agcccgagag gatgcccccc 480
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RAW SEQUENCE LISTING

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DATE: 12/07/2000

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201 gggaccgggg tgcgcagat cgggcctcc ctgcggagg ggaacaggc ggaagccctg 750
202 ggcctctccc ggcgcctcta cggggaggga taccgccga ggaagctggt ctgcggcctt 800
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204 gcccgcctcc aggcctgat cgggcctg accgcctg agagggccat ggaagcctc 900
205 gcccgcctct cggagcctt aaagctagg ggggcctcc tggaggagg gggggcctg 1020
206 gcccgcagg ccttaccga gcccagagc actccttccc cagaggtcgg ccccaagcc 1080
207 gaaagccccc cagcccgga accccuagg cgcggaggg cggccgacct ggggagcgg 1140
208 tggcggcct tctcggagg cctcagggc accctacgg ccttcgtgca ggaagccgc 1200
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212 gcccacctc ctgaagccc cgaaccccg ggcctcccg aggaggagg agggcggg 1440
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215 ccaagcaga taggggtac tggatataa 1590
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219 <211> LENGTH: 461
220 <212> TYPE: PRY
221 <213> ORGANISM: Thermus thermophilus
222 <400> SEQUENCE: 4
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225 1 5 10 15
227 Val Gly Gln Glu His Val Lys Glu Pro Leu Leu Lys Ala Ile Arg Glu
228 20 25 30
230 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
231 35 40 45
233 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
234 50 55 60
236 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
237 65 70 75 80
239 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
240 85 90 95
242 Val Glu Asp Val Arg Gln Leu Arg Glu Arg Ile His Leu Ala Pro Leu
243 100 105 110
245 Ser Ala Pro Arg Lys Val Phe Ile Leu Asp Gln Ala His Met Leu Ser
246 115 120 125
248 Lys Ser Ala Phe Asn Ala Leu Leu Lys Thr Leu Glu Glu Pro Pro Pro
249 130 135 140
251 His Val Leu Phe Val Phe Ala Thr Thr Glu Pro Gln Arg Met Pro Pro
252 145 150 155 160
254 Thr Ile Leu Ser Arg Thr Gln His Phe Arg Phe Arg Arg Leu Thr Glu
255 165 170 175
257 Glu Glu Ile Ala Phe Lys Leu Arg Arg Ile Leu Glu Ala Val Gly Arg
258 180 185 190
260 Glu Ala Gln Glu Gln Ala Leu Leu Leu Ala Arg Leu Ala Asp Gly
261 195 200 205

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:03

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Output Set: N:\CRF3\12072000\I716964.raw

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204      210      215      220
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227 235      240      245      250
269 Gly Thr Gly Val Ala Gln Ile Ala Ala Ser Leu Ala Arg Gly Lys Thr
270      245      250      255
272 Ala Glu Ala Leu Gly Leu Ala Arg Arg Leu Tyr Gly Glu Gly Tyr Ala
273      260      265      270
275 Pro Arg Ser Leu Val Ser Gly Leu Leu Glu Val Phe Arg Glu Gly Leu
276      275      280      285
278 Tyr Ala Ala Phe Gly Leu Ala Gly Thr Pro Leu Pro Ala Pro Pro Gln
279      290      295      300
281 Ala Leu Ile Ala Ala Met Thr Ala Leu Asp Glu Ala Met Glu Arg Leu
282 305      310      315      320
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295      325      330      335
297 Gly Arg Ala Leu Ala Ala Glu Ala Leu Pro Gln Pro Thr Gly Ala Pro
298      340      345      350
299 Ser Pro Glu Val Gly Pro Lys Pro Glu Ser Pro Pro Thr Pro Glu Pro
300      355      360      365
303 Pro Arg Pro Glu Glu Ala Pro Asp Leu Arg Glu Arg Trp Arg Ala Phe
304      370      375      380
306 Leu Glu Ala Leu Arg Pro Thr Leu Arg Ala Phe Val Arg Glu Ala Arg
307 385      390      395      400
309 Pro Glu Val Arg Glu Gly Gln Leu Cys Leu Ala Phe Pro Glu Asp Lys
310      405      410      415
312 Ala Phe His Tyr Arg Lys Ala Ser Glu Gln Lys Val Arg Leu Leu Pro
313      420      425      430
315 Leu Ala Gln Ala His Phe Gly Val Glu Glu Val Val Leu Val Leu Glu
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315 <210> SEQ ID NO: 5
316 <211> LENGTH: 454
317 <212> TYPE: PRI
318 <213> ORGANISM: Thermus thermophilus
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325      20      25      30
327 Gly Arg Leu Ala Gln Ala Tyr Leu Phe Ser Gly Pro Arg Gly Val Gly
328      35      40      45
330 Lys Thr Thr Thr Ala Arg Leu Leu Ala Met Ala Val Gly Cys Gln Gly
331      50      55      60
333 Glu Asp Pro Pro Cys Gly Val Cys Pro His Cys Gln Ala Val Gln Arg
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336 Gly Ala His Pro Asp Val Val Asp Ile Asp Ala Ala Ser Asn Asn Ser
337      85      90      95

```

9/7/6, 964

6

<210> 89
 <211> 182
 <212> PRT
 <213> Deinococcus radiodurans

<400> 89

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		20						25					30		
Gly	Gly	Gln	Ile	Asp	Glu	Thr	Leu	Lys	Phe	Glu	Thr	Leu	Val	Arg	Pro
		35					40					45			
Thr	Arg	Pro	Asp	Gly	Ser	Met	Leu	Ser	Ile	Pro	Trp	Gln	Ala	Gln	Arg
	50					55					60				
Val	His	Gly	Ile	Ser	Asp	Glu	Met	Val	Arg	Arg	Ala	Pro	Ala	(Xaa)	Lys
	65				70					75					80
Asp	Val	Leu	Pro	Asp	Phe	Phe	Asp	Phe	Val	Asp	Gly	Ser	Ala	Val	Val
				85					90					95	
Ala	His	Asn	Val	Ser	Phe	Asp	Gly	Gly	Phe	Met	Arg	Ala	Gly	Ala	Glu
		100						105					110		
Arg	Leu	Gly	Leu	Ser	Trp	Ala	Pro	Glu	Arg	Glu	Leu	Cys	Thr	Met	Gln
		115					120					125			
Leu	Ser	Arg	Arg	Ala	Phe	Pro	Arg	Glu	Arg	Thr	His	Asn	Leu	Thr	Val
		130					135					140			
Leu	Ala	Glu	Arg	Leu	Gly	Leu	Glu	Phe	Ala	Pro	Gly	Gly	Arg	His	Arg
	145				150					155				160	
Ser	Tyr	Gly	Asp	Val	Gln	Val	Thr	Ala	Gln	Ala	Tyr	Leu	Arg	Leu	Leu
			165						170					175	
Glu	Leu	Leu	Gly	Glu	Arg										
			180												

all item 10
 on Enon
 summary
 sheet

FYI:

Please Note:

Us of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/716,964

DATE: 12/07/2000

TIME: 07:50:04

Input Set : A:\R10301.app

Output Set: N:\CRF3\12072000\I716964.raw

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:1552 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:17
L:1552 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:17
L:1552 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:1062 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:29
L:1062 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:29
L:1062 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:29
L:1074 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:30
L:1074 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:30
L:1074 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:30
L:1224 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42
L:1232 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43
L:1506 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:66
L:1506 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:66
L:1506 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:66
L:1519 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:67
L:1519 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:67
L:1519 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:67
L:1532 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:68
L:1532 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:68
L:1532 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:68
L:2169 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:89
L:2169 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:89
L:2169 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:89
L:2169 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:89
L:2169 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:89
L:2252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:2252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:2252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:2252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
L:2252 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:91
L:2255 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:91
M:340 Repeated in SeqNo=91